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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/043,774BDATE: 06/17/2002
TIME: 14:44:59Input Set: A:\02-0013.st25.txt
Output Set: N:\CRF3\06172002\J043774B.raw

3 <110> APPLICANT: University of Illinois at Chicago
 4 Sharma, Arun
 5 Hoffman, Ronald
 7 <120> TITLE OF INVENTION: HUMAN HEMATOPOIETIC GROWTH REGULATORY GENE AND USES
 9 <130> FILE REFERENCE: MBHB: CU08/PPA
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/043,774B
 C--> 11 <141> CURRENT FILING DATE: 2002-06-06
 11 <160> NUMBER OF SEQ ID NOS: 17
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 2328
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(2328)
 23 <223> OTHER INFORMATION: Human Hiwi Protein
 26 <400> SEQUENCE: 1
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 28 Met Ile Phe Gly Val Asn Thr Arg Gln Asn Leu Asp His Val Lys Glu
 29 1 5 10 15
 31 tca aaa aca ggt tct tca ggc att ata gta agg tta agc act aac cat 96
 32 Ser Lys Thr Gly Ser Ser Gly Ile Ile Val Arg Leu Ser Thr Asn His
 33 20 25 30
 35 ttc cgg ctg aca tcc cgt ccc cag tgg gcc tta tat cag tat cac att 144
 36 Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile
 37 35 40 45
 39 gac tat aac cca ctg atg gaa gcc aga aga ctc cgt tca gct ctt ctt 192
 40 Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu
 41 50 55 60
 43 ttt caa cac gaa gat cta att gga aag tgt cat gct ttt gat gga acg 240
 44 Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr
 45 65 70 75 80
 47 ata tta ttt tta cct aaa aga cta cag caa aag gtt act gaa gtt ttt 288
 48 Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe
 49 85 90 95
 51 agt aag acc cgg aat gga gag gat gtg agg ata acg atc act tta aca 336
 52 Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr
 53 100 105 110
 55 aat gaa ctt cca cct aca tca cca act tgt ttg cag ttc tat aat att 384
 56 Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile
 57 115 120 125
 59 att ttc agg agg ctt ttg aaa atc atg aat ttg caa caa att gga cga 432

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60	Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg			
61	130	135	140	
63	aat tat tat aac cca aat gac cca att gat att cca agt cac agg ttg		480	
64	Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp Ile Pro Ser His Arg Leu			
65	145	150	155	160
67	gtg att tgg cct ggc ttc act act tcc atc ctt cag tat gaa aac agc		528	
68	Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser			
69	165	170	175	
71	atc atg ctc tgc act gac gtt agc cat aaa gtc ctt cga agt gag act		576	
72	Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr			
73	180	185	190	
75	gtt ttg gat ttc atg ttc aac ttt tat cat cag aca gaa gaa cat aaa		624	
76	Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys			
77	195	200	205	
79	ttt caa gaa caa gtt tcc aaa gaa cta ata ggt tta gtt gtt ctt acc		672	
80	Phe Gln Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr			
81	210	215	220	
83	aag tat aac aat aag aca tac aga gtg gat gat att gac tgg gac cag		720	
84	Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln			
85	225	230	235	240
87	aat ccc aag agc acc ttt aag aaa gcc gac ggc tct gaa gtc agc ttc		768	
88	Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe			
89	245	250	255	
91	tta gaa tac tac agg aag caa tac aac caa gag atc acc gac ttg aag		816	
92	Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys			
93	260	265	270	
95	cag cct gtc ttg gtc agc cag ccc aag aga agg cgg ggc cct ggg ggg		864	
96	Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Gly Pro Gly Gly			
97	275	280	285	
99	aca ctg cca ggg cct gcc atg ctc att cct gag ctc tgc tat ctt aca		912	
100	Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr			
101	290	295	300	
103	ggt cta act gat aaa atg cgt aat gat ttt aac gtg atg aaa gac tta		960	
104	Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu			
105	305	310	315	320
107	gcc gtt cat aca aga cta act cca gag caa agg cag cgt gaa gtg gga		1008	
108	Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly			
109	325	330	335	
111	cga ctc att gat tac att cat aaa aac gat aat gtt caa agg gag ctt		1056	
112	Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu			
113	340	345	350	
115	cga gac tgg ggt ttg agc ttt gat tcc aac tta ctg tcc ttc tca gga		1104	
116	Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly			
117	355	360	365	
119	aga att ttg caa aca gaa aag att cac caa ggt gga aaa aca ttt gat		1152	
120	Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp			
121	370	375	380	
123	tac aat cca caa ttt gca gat tgg tcc aaa gaa aca aga ggt gca cca		1200	
124	Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro			

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125	385	390	395	400	
127	tta att agt gtt aag cca cta gat aac tgg ctg ttg atc tat acg cga				1248
128	Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg				
129	405	410	415		
131	aga aat tat gaa gca gcc aat tca ttg ata caa aat cta ttt aaa gtt				
132	Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val				1296
133	420	425	430		
135	aca cca gcc atg ggc atg caa atg aga aaa gca ata atg att gaa gtg				
136	Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val				1344
137	435	440	445		
139	gat gac aga act gaa gcc tac tta aga gtc tta cag caa aag gtc aca				
140	Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr				1392
141	450	455	460		
143	gca gac acc cag ata gtt gtc tgt ctg ttg tca agt aat cgg aag gac				
144	Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp				1440
145	465	470	475	480	
147	aaa tac gat gct att aaa aaa tac ctg tgt aca gat tgc cct acc cca				
148	Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro				1488
149	485	490	495		
151	agt cag tgt gtg gtc cga acc tta ggc aaa cag caa act gtc atg				
152	Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met				1536
153	500	505	510		
155	gcc att gct aca aag att gcc cta cag atg aac tgc aag atg gga gga				
156	Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly				1584
157	515	520	525		
159	gag ctc tgg agg gtg gac atc ccc ctg aag ctc gtg atg atc gtt ggc				
160	Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly				1632
161	530	535	540		
163	atc gat tgt tac cat gac atg aca gct ggg cgg agg tca atc gca gga				
164	Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly				1680
165	545	550	555	560	
167	ttt gtt gcc agc atc aat gaa ggg atg acc cgc tgg ttc tca cgc tgc				
168	Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys				1728
169	565	570	575		
171	ata ttt cag gat aga gga cag gag ctg gta gat ggg ctc aaa gtc tgc				
172	Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys				1776
173	580	585	590		
175	ctg caa gcg gct ctg agg gct tgg aat agc tgc aat gag tac atg ccc				
176	Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro				1824
177	595	600	605		
179	agc cgg atc atc gtg tac cgc gat ggc gta gga gac ggc cag ctg aaa				
180	Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys				1872
181	610	615	620		
183	aca ctg gtg aac tac gaa gtg cca cag ttt ttg gat tgt cta aaa tcc				
184	Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser				1920
185	625	630	635	640	
187	att ggt aga ggt tac aac cct aga cta acg gta att gtg gtg aag aaa				
188	Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys				1968
189	645	650	655		

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191	aga	gtg	aac	acc	aga	ttt	ttt	gct	cag	tct	gga	gga	aga	ctt	cag	aat		2016	
192	Arg	Val	Asn	Thr	Arg	Phe	Phe	Ala	Gln	Ser	Gly	Gly	Arg	Leu	Gln	Asn			
193									660		665					670			
195	cca	ctt	cct	gga	aca	gtt	att	gat	gta	gag	gtt	acc	aga	cca	gaa	tgg		2064	
196	Pro	Leu	Pro	Gly	Thr	Val	Ile	Asp	Val	Glu	Val	Thr	Arg	Pro	Glu	Trp			
197									675		680					685			
199	tat	gac	ttt	ttt	atc	gtg	agc	cag	gct	gtg	aga	agt	gtt	agt	gtt	tct		2112	
200	Tyr	Asp	Phe	Phe	Ile	Val	Ser	Gln	Ala	Val	Arg	Ser	Gly	Ser	Val	Ser			
201									690		695					700			
203	ccc	aca	cat	tac	aat	gtc	atc	tat	gac	aac	agc	ggc	ctg	aag	cca	gac		2160	
204	Pro	Thr	His	Tyr	Asn	Val	Ile	Tyr	Asp	Asn	Ser	Gly	Leu	Lys	Pro	Asp			
205	705								710				715			720			
207	cac	ata	cag	cgc	ttg	acc	tac	aag	ctg	tgc	cac	atc	tat	tac	aac	tgg		2208	
208	His	Ile	Gln	Arg	Leu	Thr	Tyr	Lys	Leu	Cys	His	Ile	Tyr	Tyr	Asn	Trp			
209									725		730					735			
211	cca	ggt	gtc	att	cgt	gtt	cct	gct	cct	tgc	cag	tac	gcc	cac	aag	ctg		2256	
212	Pro	Gly	Val	Ile	Arg	Val	Pro	Ala	Pro	Cys	Gln	Tyr	Ala	His	Lys	Leu			
213									740		745					750			
215	gct	ttt	ctt	gtt	ggc	cag	agt	att	cac	aga	gag	cca	aat	ctg	tca	ctg		2304	
216	Ala	Phe	Leu	Val	Gly	Gln	Ser	Ile	His	Arg	Glu	Pro	Asn	Leu	Ser	Leu			
217									755		760					765			
219	tca	aac	cgc	ctt	tac	tac	ctc	taa										2328	
220	Ser	Asn	Arg	Leu	Tyr	Tyr	Leu												
221									770		775								
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225	<211>	LENGTH:	775																
226	<212>	TYPE:	PRT																
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235	Ser	Lys	Thr	Gly	Ser	Ser	Gly	Ile	Ile	Val	Arg	Leu	Ser	Thr	Asn	His			
236								20		25					30				
239	Phe	Arg	Leu	Thr	Ser	Arg	Pro	Gln	Trp	Ala	Leu	Tyr	Gln	Tyr	His	Ile			
240							35		40						45				
243	Asp	Tyr	Asn	Pro	Leu	Met	Glu	Ala	Arg	Arg	Leu	Arg	Ser	Ala	Leu	Leu			
244							50		55						60				
247	Phe	Gln	His	Glu	Asp	Leu	Ile	Gly	Lys	Cys	His	Ala	Phe	Asp	Gly	Thr			
248							65		70						75			80	
251	Ile	Leu	Phe	Leu	Pro	Lys	Arg	Leu	Gln	Gln	Lys	Val	Thr	Glu	Val	Phe			
252								85		90					95				
255	Ser	Lys	Thr	Arg	Asn	Gly	Glu	Asp	Val	Arg	Ile	Thr	Ile	Thr	Leu	Thr			
256								100		105					110				
259	Asn	Glu	Leu	Pro	Pro	Thr	Ser	Pro	Thr	Cys	Leu	Gln	Phe	Tyr	Asn	Ile			
260								115		120					125				
263	Ile	Phe	Arg	Arg	Leu	Leu	Lys	Ile	Met	Asn	Leu	Gln	Gln	Ile	Gly	Arg			
264								130		135					140				
267	Asn	Tyr	Tyr	Asn	Pro	Asn	Asp	Pro	Ile	Asp	Ile	Pro	Ser	His	Arg	Leu			
268								145		150					155			160	

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271 Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser
272 165 170 175
275 Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr
276 180 185 190
279 Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys
280 195 200 205
283 Phe Gln Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr
284 210 215 220
287 Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln
288 225 230 235 240
291 Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe
292 245 250 255
295 Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys
296 260 265 270
299 Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg Gly Pro Gly Gly
300 275 280 285
303 Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr
304 290 295 300
307 Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu
308 305 310 315 320
311 Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly
312 325 330 335
315 Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu
316 340 345 350
319 Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly
320 355 360 365
323 Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Lys Thr Phe Asp
324 370 375 380
327 Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro
328 385 390 395 400
331 Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg
332 405 410 415
335 Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val
336 420 425 430
339 Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val
340 435 440 445
343 Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr
344 450 455 460
347 Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp
348 465 470 475 480
351 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro
352 485 490 495
355 Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met
356 500 505 510
359 Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly
360 515 520 525
363 Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly
364 530 535 540
367 Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly

VERIFICATION SUMMARY

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Input Set : A:\02-0013.st25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date